FIG. 1

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FIG. 2

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FIG. 3

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FIG. 4

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FIG. 5

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FIG. 6

O.D. 630nm

Dilution

-o- CH 563 3hr
-•- CH 563 3hr + A2
-△- CH 563 16hr
-▲- CH 563 16hr + A2

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FIG. 7

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FIG. 8A

FIG. 8B

FIG. 9A

FIG. 9B

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$$y = 7.0802 - 5.9612 \text{ x} \quad R^2 = 0.944$$

I-125 murine A2 IgG
Estimated Avg. Ka = 0.5 x 10^9

ng Bound/(Free) x 10^8

ng Bound

FIG. 10A

$$y = 25.953 - 15.306 \text{ x} \quad R^2 = 0.972$$

I-125 chimeric A2 IgG
Estimated Avg. Ka = 1.8 x 10^9

ng Bound/(Free) x 10^8

ng Bound

FIG. 10B

08/192,86?

FIG. 11

FIG. 12

```
1
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
                                  10
21
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly
                                  30
41
Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser
                                  50
61
Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
                                  70
81
Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
                                  90
101
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
                                  110
121
Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp
                                  130
141
Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
                                  150
```

FIG. 13

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FIG. 14A

FIG. 14B

1
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
10

21
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly
30

41
Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser
50

61
Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
70

81
Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
90

101
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
110

121
Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp
130

141
Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
150

FIG. 15

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGAGAAAGAGTCAGT
AspIleLeuLeuThrGlnSerProAlaIleLeuSerValSerProGlyGluArgValSer

TTCTCCTGCAGGGCCAGTCAGTTCGTTGGCTCAAGCATCCACTGGTATCAGCAAAGAACA
PheSerCysArgAlaSerGlnPheValGlySerSerIleHisTrpTyrGlnGlnArgThr

AATGGTTCTCCAAGGCTTCTCATAAAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCC
AsnGlySerProArgLeuLeuIleLysTyrAlaSerGluSerMetSerGlyIleProSer

AGGTTTAGTGGCAGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT
ArgPheSerGlySerGlySerGlyThrAspPheThrLeuSerIleAsnThrValGluSer

GAAGATATTGCAGATTATTACTGTCAAGAAAGTCATAGCTGGCCATTCACGTTCGGCTCG
GluAspIleAlaAspTyrTyrCysGlnGluSerHisSerTrpProPheThrPheGlySer

GGGACAAATTTGGAAGTAAAA
GlyThrAsnLeuGluValLys

FIG. 16A

GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGTGCAACCTGGAGGATCCATGAAACTC
GluValLysLeuGluGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu

TCCTGTGTTGCCTCTGGATTCATTTCAGTAACCACTACTGGATGAACTGGGTCCGCCAGTCT
SerCysValAlaSerGlyPheIlePheSerAsnHisTrpMetAsnTrpValArgGlnSer

CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGATCAAAAATCTATTAATTCTGCAACA
ProGluLysGlyLeuGluTrpValAlaGluIleArgSerLysSerIleAsnSerAlaThr

CATTATGCGGAGTCTGTGAAAGGGGAGGTTCACCATCTCAAGAGATGATTCCAAAAGTGCT
HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspAspSerLysSerAla

GTGTACCTGCAAATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTCCAGG
ValTyrLeuGlnMetThrAspLeuArgThrGluAspThrGlyValTyrTyrCysSerArg

AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTCACAGTGTCC
AsnTyrTyrGlySerThrTyrAspTyrTrpGlyGlnGlyThrThrLeuThrValSer

FIG. 16B

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PAIN

Patient Number
□— 1-15
■— 6-9

Percent of Day 1

Day

FIG. 18

EMS

Patient Number
□— 1-5
■— 6-9

Percent of Day 1

Day

FIG. 17

SWOLLEN JOINTS

Percent of Day 1

Patient Number

□ 1-5

■ 6-9

Day

FIG. 20

RITCHIE ARTICULAR INDEX

Percent of Day 1

Patient Number

□ 1-5

■ 6-9

Day

FIG. 19

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ESR

Percent of Day 1

Day

Patient Number
- 1-5
- 6-8

FIG. 22

CRP

Percent of Day 1

Day

Patient Number
- 2-5
- 6,8-9

FIG. 21

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FIG. 23

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FIG. 24

Swollen Joint Count (0-28)

Weeks

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FIG. 25

CRP (mg/l)

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FIG. 26A

Heavy chain fusion genes

Igh promoter

Igh leader

TNfR

J

CH1 CH2 CH3

hg

Δsf3

JCκ gene

Ig kappa promoter

Ig kappa leader

J

EcoRV

Cκ

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FIG. 26B

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FIG. 27

PCR fragments

rev ⟶ ⟵ for

M-T412 IgH gene

```
Eco  Stu        Xba    Xba Eco  pUC19
```

pHC584

```
Eco  Stu        Stu  Xba Xba Eco  pUC19
```

```
Stu  Xba Xba  pUC19
```

pHC707

partial sequence of pHC707
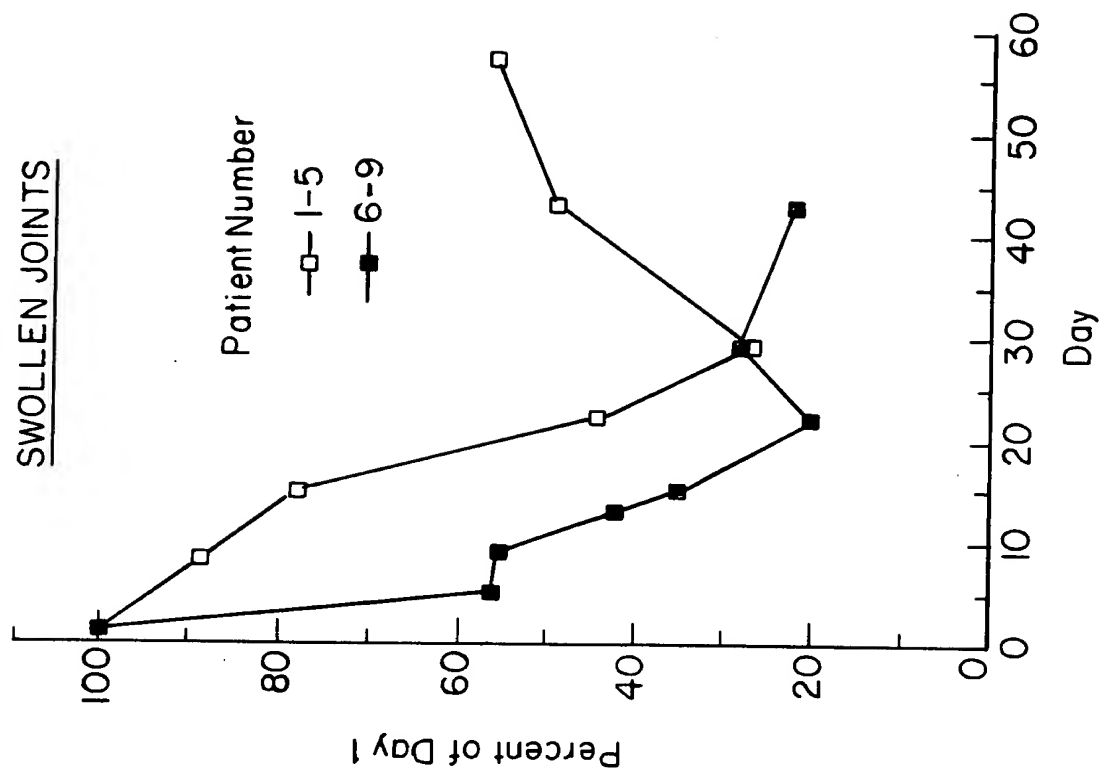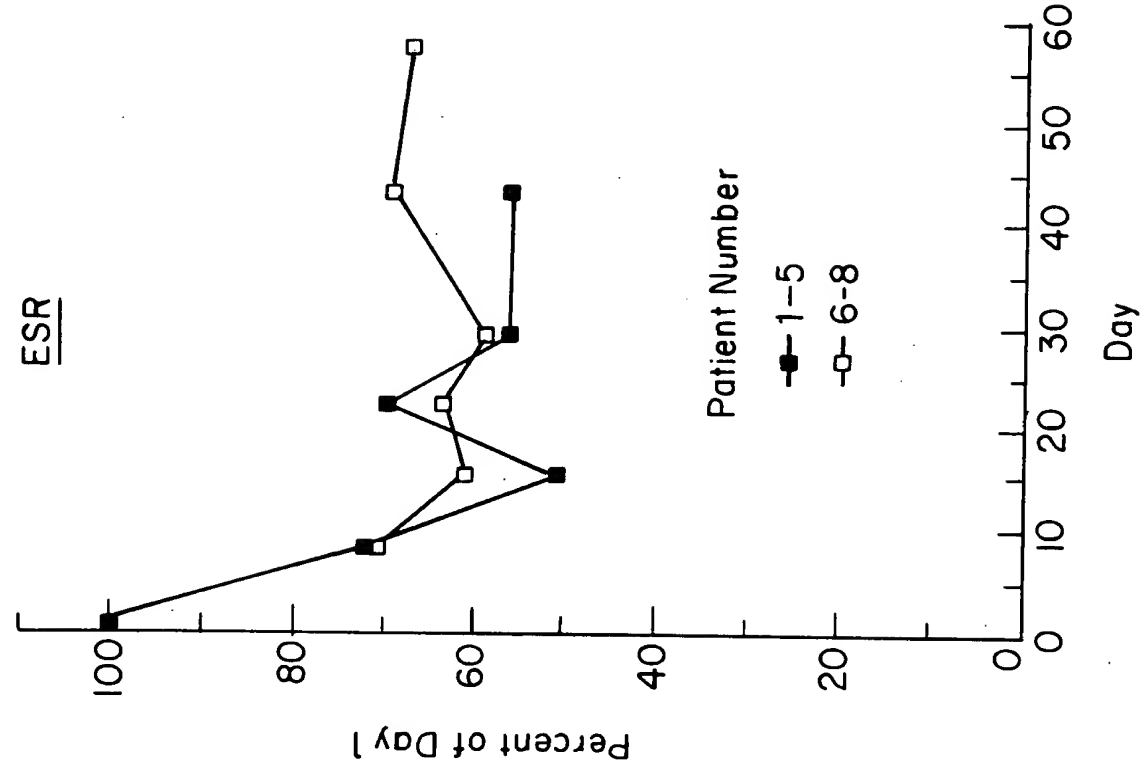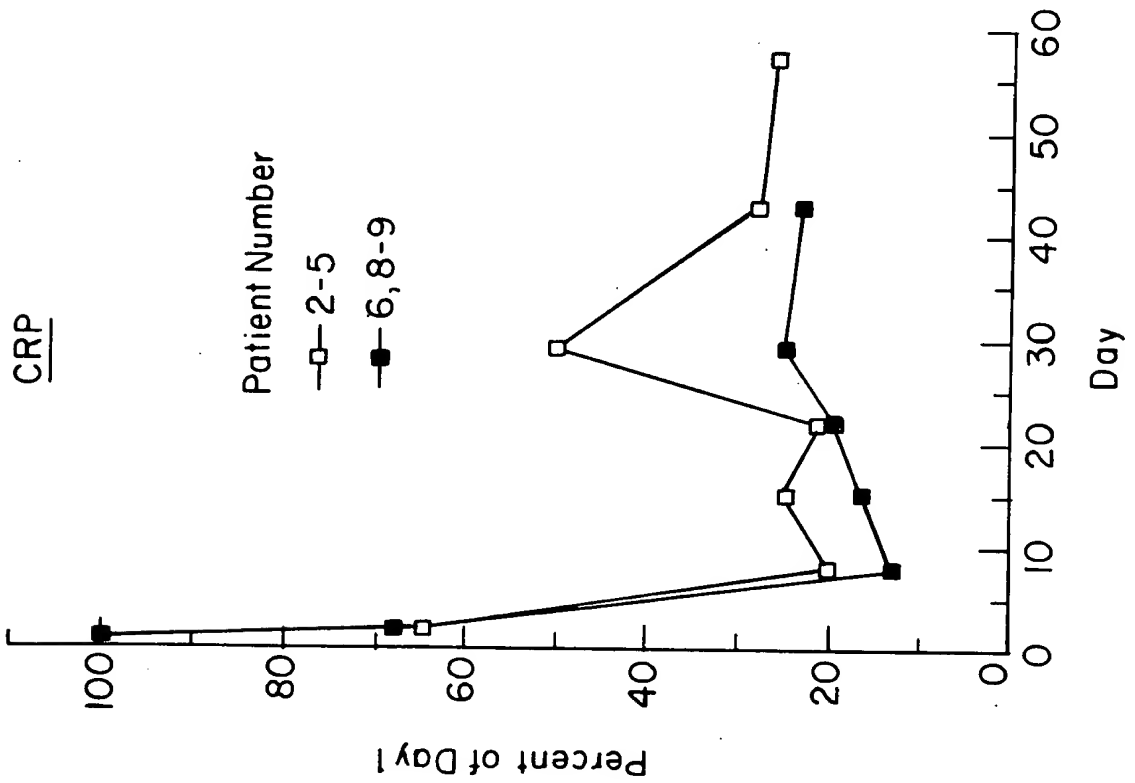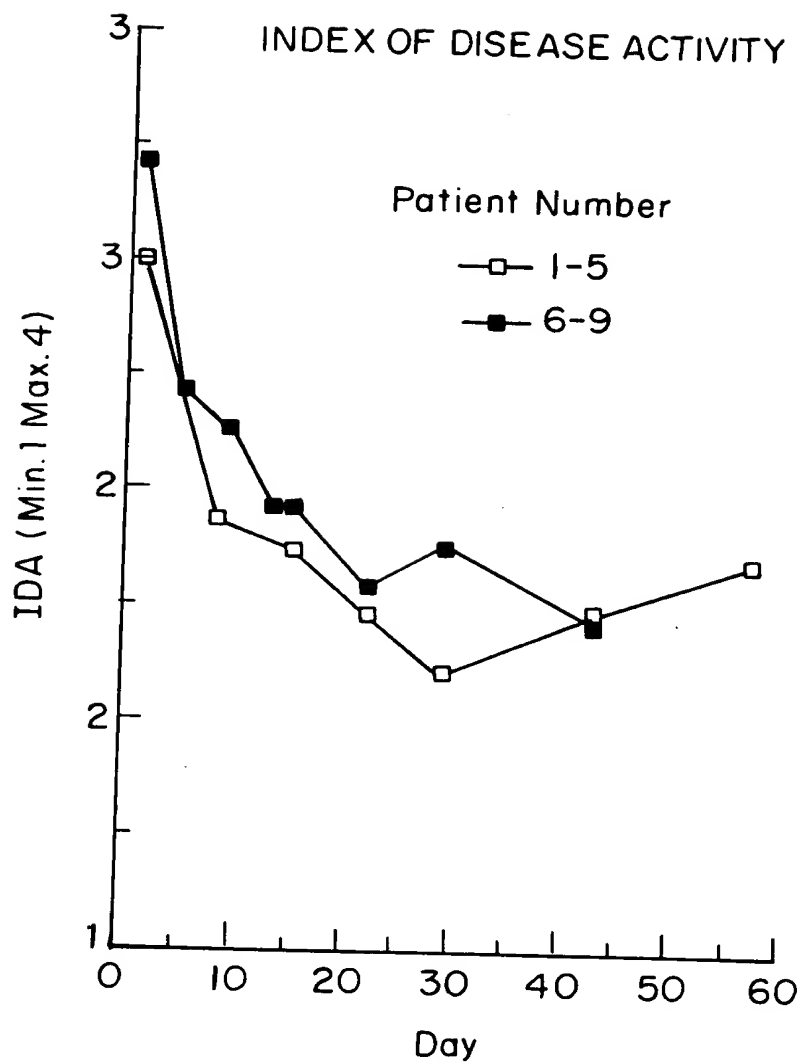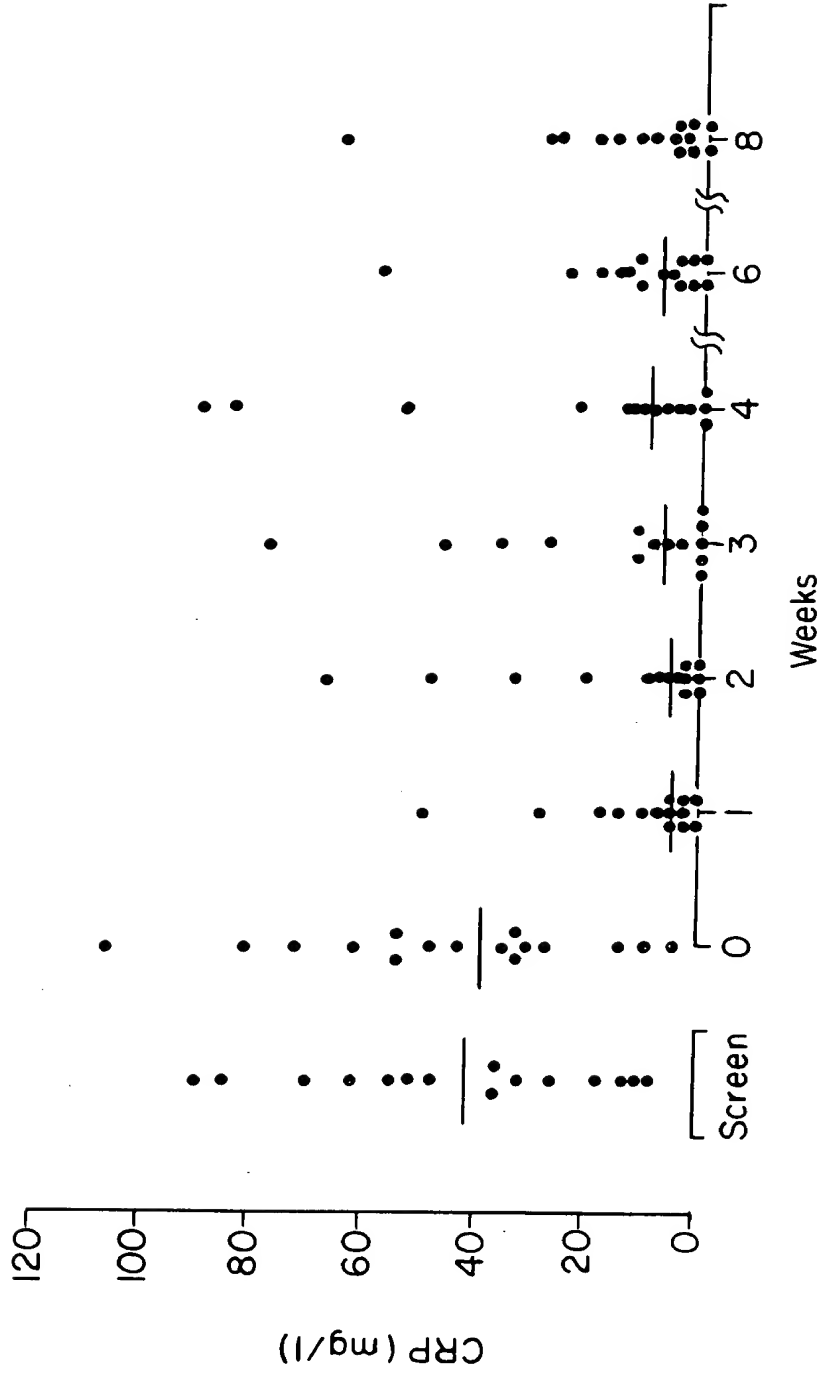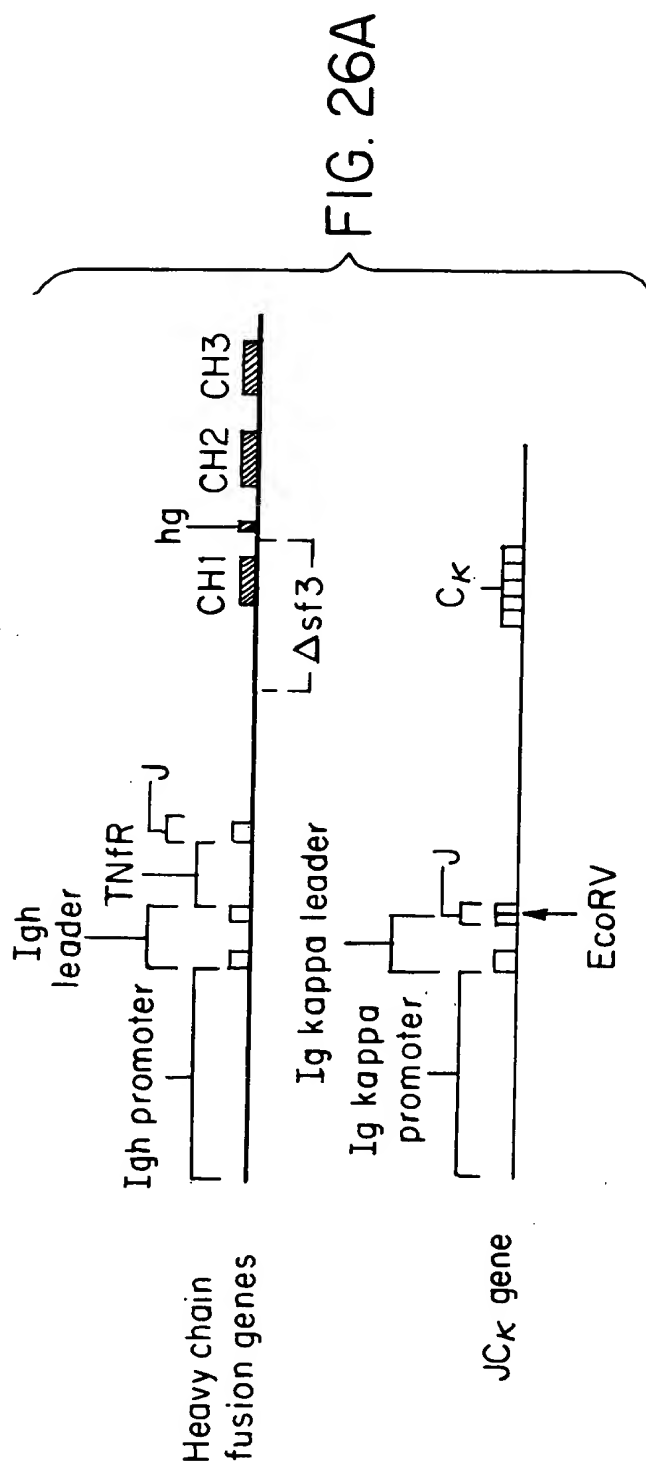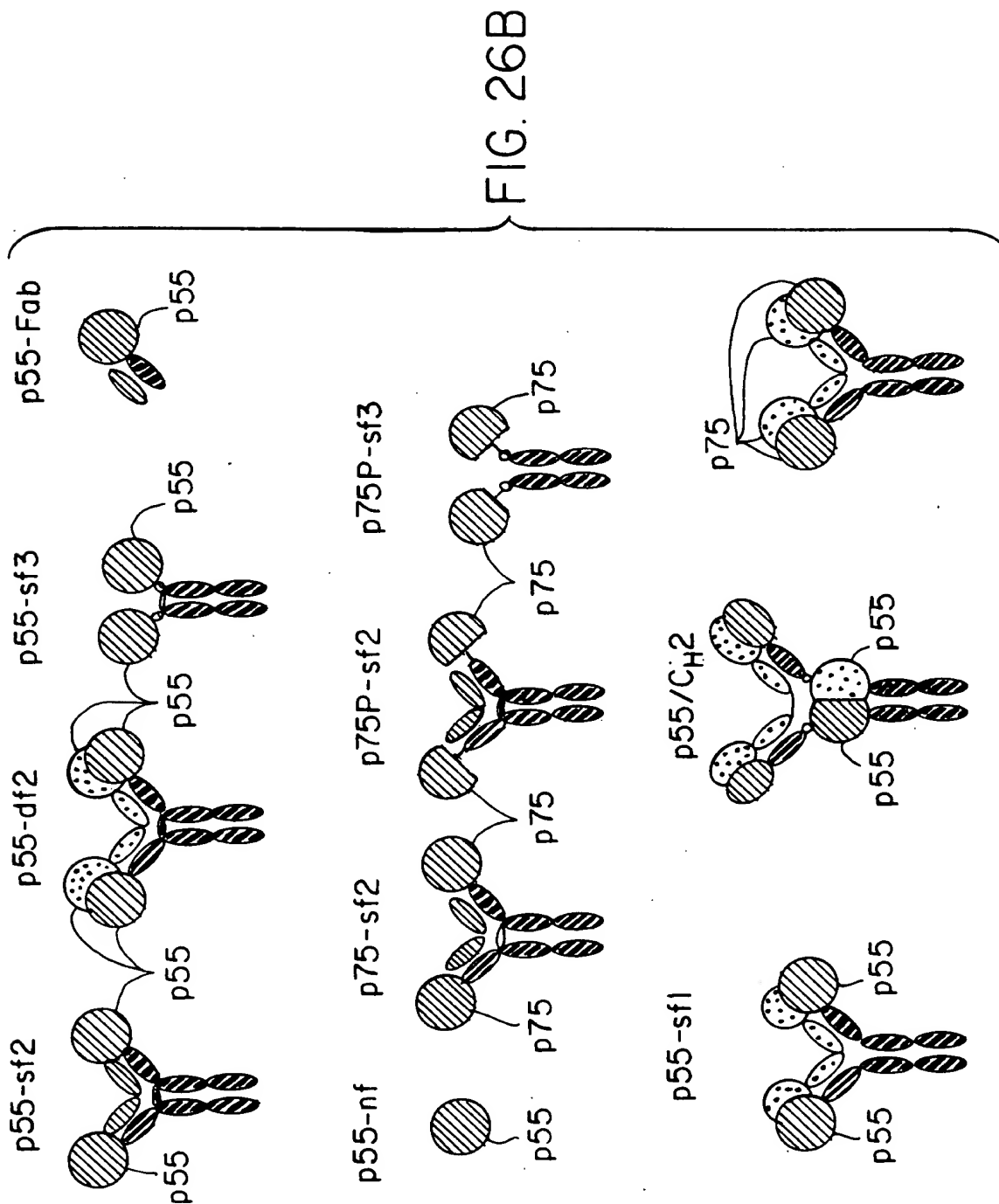
leader intron | incomplete leader peptide | human J | J-C intron

Ite Glu | Pro Gly Thr Leu Val Thr Val Ser Ser

CACAG GT ATC CAG G CCT GGT ACC TTA GTC ACC GTC TCC TCA G GTAA

Stu

pHC707 with insert

Signal peptidase

leader intron | leader peptide | human J | J-C intron

Ite Glu Ala | Pro Gly Thr Leu Val Thr Val Ser Ser

CACAG GT ATC CAG G CA......CCT GGT ACC TTA GTC ACC GTC TCC TCA G GTAA

insert

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FIG. 28

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PCR fragments

rev ←
← for

M-T4l2 light
chain gene

Hd   Hd
pUCl9

PV

Hd   Hd
pUCl9

pLC67l

partial
sequence
of pLC87l

Signal peptidase →

leader
intron

leader peptide

Val Glu Gly Asp Ile Gly Thr Lys Leu Glu Ile Lys

TTTGCAG GT GTT GAA GGA GAT ATC GGG ACA AAG TTG GAA ATA AAA C GTAAGT

RV

human J

J-C
intron

pLC67l
with insert

Signal peptidase →

leader
intron

leader peptide

Val Glu Gly Asp   Ile Gly Thr Lys Leu Glu Ile Lys

TTTGCAG GT GTT GAA GGA GAT.......ATC GGG ACA AAG TTG GAA ATA AAA C GTAAGT

insert

human J

J-C
intron

FIG. 29

FIG. 30

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FIG. 31A

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FIG. 31B

FIG. 31C

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FIG. 32

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FIG. 33A

FIG. 33B

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p55-df2

y=102.51-1.6608e-2x
R^2=0.981

bound (cpm)

bound (cpm)/Free (pm)

FIG. 33D

p55-sf2

y=97.625-1.7489e-2x
R^2=0.963

bound (cpm)

bound (cpm)/Free (pm)

FIG. 33C

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p75 - sf2

y=196.56-2.9952e-2x
R^2=0.981

bound (cpm)

bound (cpm)/Free (pm)

200

100

0

0   2000   4000   6000

FIG. 33F

p55-sf3

y=109.39-2.0858e-2x
R^2=0.954

bound (cpm)

bound (cpm)/Free (pm)

120

100

80

60

40

20

0

0   2000   4000

FIG. 33E

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p75P-sf3

$y = 193.31 - 7.3370e-2x$
$R^2 = 0.972$

bound (cpm)/Free (pm)

bound (cpm)

FIG. 33H

p75P-sf2

$y = 236.42 - 3.4611e-2x$
$R^2 = 0.967$

bound (cpm)/Free (pm)

bound (cpm)

FIG. 33G